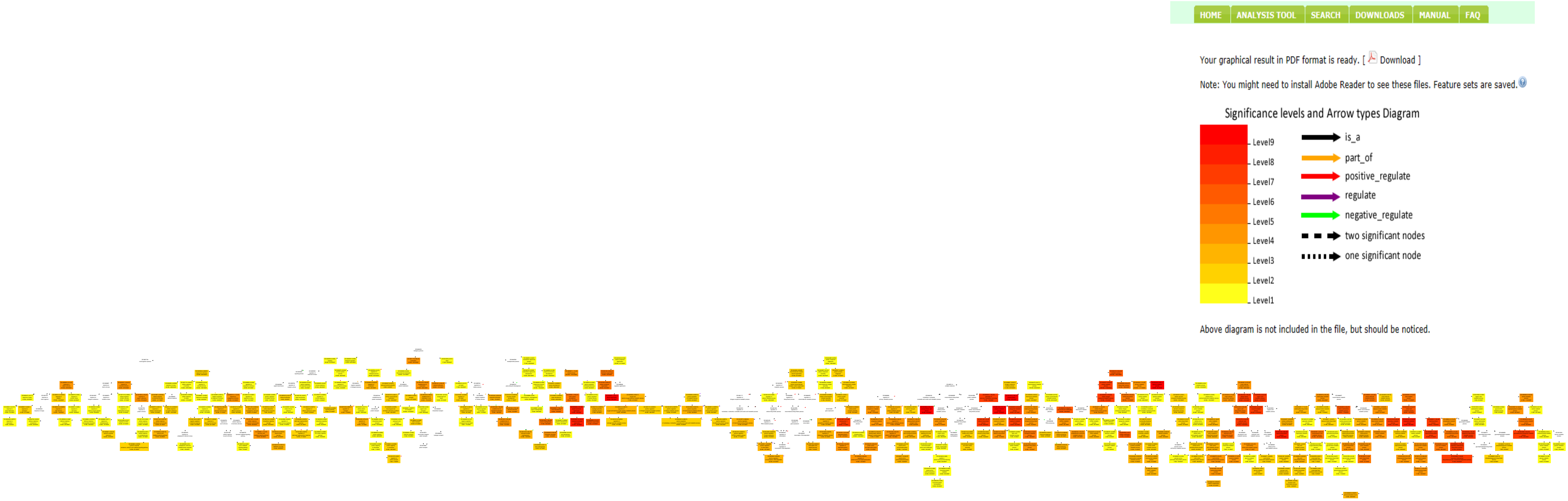

Your graphical result in PDF format is ready. [Download]

Note: You might need to install Adobe Reader to see these files. Feature sets are saved.

Above diagram is not included in the file, but should be noticed.

Fig. S4. Gene ontology (GO) analysis of upregulated genes in *NbRPL10A*-silenced samples when compared to vector control (VC) samples without any pathogen treatment. The differentially expressed genes from RNA seq data of *N. benthamiana* were used for BLAST analysis to find Arabidopsis homologs and the unigenes from Arabidopsis were submitted to pathway analysis using agriGo analysis tool (http://bioinfo.cau.edu.cn/agriGO/).